

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/549,506
Source: IFWP
Date Processed by STIC: 11/16/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 11/16/2006

PATENT APPLICATION: US/10/549,506

TIME: 11:03:32

Input Set : A:\0272wo310.ST25.txt

Output Set: N:\CRF4\11162006\J549506.raw

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3 <110> APPLICANT: Maxygen ApS
4   Maxygen Holdings Ltd.
5   Haaning, Jesper Mortensen
6   Andersen, Kim Vilbour
7   Roepke, Mads
8   Glazer, Steven
10 <120> TITLE OF INVENTION: FVII or FVIIa Variants
12 <130> FILE REFERENCE: 0272wo310
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/549,506
C--> 14 <141> CURRENT FILING DATE: 2005-09-16
14 <150> PRIOR APPLICATION NUMBER: US 60/456,547
15 <151> PRIOR FILING DATE: 2003-03-20
17 <150> PRIOR APPLICATION NUMBER: US 60/479,708
18 <151> PRIOR FILING DATE: 2003-06-19
20 <160> NUMBER OF SEQ ID NOS: 19
22 <170> SOFTWARE: PatentIn version 3.2
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1338
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (115)..(1338)
34 <400> SEQUENCE: 1
35 atgggtcagcc aggcctccg cctcctgtgc ctgctcctgg ggctgcaggg ctgcctggct      60
37 gccgtcttcg tcaccagga ggaagccat ggcgtcctgc atcgccggcg ccgg gcc      117
38                                     Ala
39                                     1
41 aat gcc ttt ctg gaa gag ctc cgc cct ggc tcc ctg gaa cgc gaa tgc      165
42 Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys
43           5                10                15
45 aaa gag gaa cag tgc agc ttt gag gaa gcc cgg gag att ttc aaa gac      213
46 Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp
47           20                25                30
49 gct gag cgg acc aaa ctg ttt tgg att agc tat agc gat ggc gat cag      261
50 Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln
51           35                40                45
53 tgc gcc tcc agc cct tgc cag aac ggg ggc tcc tgc aaa gac cag ctg      309
54 Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu
55 50                55                60                65
57 cag agc tat atc tgc ttc tgc ctg cct gcc ttt gag ggg cgc aat tgc      357
58 Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys
59           70                75                80

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61	gaa acc cat aag gat gac cag ctg att tgc gtc aac gaa aac ggg ggc	405
62	Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly Gly	
63	85 90 95	
65	tgc gag cag tac tgc agc gat cac acg ggc acg aag cgg agc tgc cgc	453
66	Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys Arg	
67	100 105 110	
69	tgc cac gaa ggc tat agc ctc ctg gct gac ggg gtg tcc tgc acg ccc	501
70	Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro	
71	115 120 125	
73	acg gtg gaa tac cct tgc ggg aag att ccc att cta gaa aag cgg aac	549
74	Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn	
75	130 135 140 145	
77	gct agc aaa ccc cag ggc cgg atc gtc ggc ggg aag gtc tgc cct aag	597
78	Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys	
79	150 155 160	
81	ggg gag tgc ccc tgg cag gtc ctg ctc ctg gtc aac ggg gcc cag ctg	645
82	Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln Leu	
83	165 170 175	
85	tgc ggc ggg acc ctc atc aat acc att tgg gtc gtg tcc gcc gct cac	693
86	Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala His	
87	180 185 190	
89	tgc ttc gat aag att aag aat tgg cgg aac ctc atc gct gtg ctc ggc	741
90	Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu Gly	
91	195 200 205	
93	gaa cac gat ctg tcc gag cat gac ggg gac gaa cag tcc cgc cgg gtg	789
94	Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Val	
95	210 215 220 225	
97	gct cag gtc atc att ccc tcc acc tat gtg cct ggc acg acc aat cac	837
98	Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His	
99	230 235 240	
101	gat atc gct ctg ctc cgc ctc cac cag ccc gtc gtg ctc acc gat cac	885
102	Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His	
103	245 250 255	
105	gtc gtg cct ctg tgc ctg cct gag cgg acc ttt agc gaa cgc acg ctg	933
106	Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu	
107	260 265 270	
109	gct ttc gtc cgc ttt agc ctc gtg tcc ggc tgg ggc cag ctg ctc gac	981
110	Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu Asp	
111	275 280 285	
113	cgg ggc gct acc gct ctc gag ctg atg gtg ctc aac gtc ccc cgg ctg	1029
114	Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg Leu	
115	290 295 300 305	
117	atg acc cag gac tgc ctg cag cag tcc cgc aaa gtg ggg gac tcc ccc	1077
118	Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser Pro	
119	310 315 320	
121	aat atc acg gag tat atg ttt tgc gct ggc tat agc gat ggc tcc aag	1125
122	Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser Lys	
123	325 330 335	
125	gat agc tgc aag ggg gac tcc ggc ggg ccc cat gcc acg cac tat cgc	1173

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126 Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg
127          340          345          350
129 ggg acc tgg tac ctc acc ggg atc gtc agc tgg ggc cag ggc tgc gcc      1221
130 Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala
131          355          360          365
133 acg gtg ggg cac ttt ggc gtc tac acg cgc gtc agc cag tac att gag      1269
134 Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu
135 370          375          380          385
137 tgg ctg cag aag ctc atg cgg agc gaa ccc cgg ccc ggg gtg ctc ctg      1317
138 Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu Leu
139          390          395          400
141 cgg gcc cct ttc cct tga taa      1338
142 Arg Ala Pro Phe Pro
143          405
146 <210> SEQ ID NO: 2
147 <211> LENGTH: 406
148 <212> TYPE: PRT
149 <213> ORGANISM: Homo sapiens
151 <400> SEQUENCE: 2
153 Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu
154 1          5          10          15
157 Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys
158          20          25          30
161 Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp
162          35          40          45
165 Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
166          50          55          60
169 Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn
170 65          70          75          80
173 Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly
174          85          90          95
177 Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys
178          100          105          110
181 Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr
182          115          120          125
185 Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg
186          130          135          140
189 Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro
190 145          150          155          160
193 Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln
194          165          170          175
197 Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala
198          180          185          190
201 His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu
202          195          200          205
205 Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg
206          210          215          220
209 Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn
210 225          230          235          240

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213 His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp
214                      245                      250                      255
217 His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr
218                      260                      265                      270
221 Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu
222                      275                      280                      285
225 Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg
226                      290                      295                      300
229 Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser
230 305                      310                      315                      320
233 Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser
234                      325                      330                      335
237 Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr
238                      340                      345                      350
241 Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys
242                      355                      360                      365
245 Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile
246                      370                      375                      380
249 Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu
250 385                      390                      395                      400
253 Leu Arg Ala Pro Phe Pro
254                      405

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257 <210> SEQ ID NO: 3

258 <211> LENGTH: 1357

259 <212> TYPE: DNA

260 <213> ORGANISM: Artificial

262 <220> FEATURE:

263 <223> OTHER INFORMATION: Synthetic gene for optimized expression of hFVII

265 <400> SEQUENCE: 3

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266 ggatcccgcc accatgggtca gccaggcctt ccgcctcctg tgctgtctcc tggggctgca      60
268 gggctgcctg gctgccgtct tcgtcaccga ggaggaagcc catggcgctc tgcacgcgcg      120
270 gcgcccggggc aatgcctttc tggaagagct ccgccctggc tccctggaac gcgaatgcaa      180
272 agaggaacacg tgcagctttg aggaagcccg ggagattttc aaagacgctg agcggaccaa      240
274 actgttttgg attagctata gcgatggcga tcagtgcgcc tccagccctt gccagaacgg      300
276 gggctcctgc aaagaccagc tgcagagcta tatctgcttc tgctgcctg cctttgaggg      360
278 gcgcaattgc gaaaccata aggatgacca gctgatttgc gtcaacgaaa acgggggctg      420
280 cgagcagtac tgcagcgatc acacgggcac gaagcggagc tgccgctgcc acgaaggcta      480
282 tagcctcctg gctgacgggg tgtcctgcac gccacgggtg gaataccctt gcgggaagat      540
284 tcccattcta gaaaagcgga acgctagcaa accccagggc cggatcgctc gcgggaaggt      600
286 ctgccctaag ggggagtgcc cctggcaggt cctgctcctg gtcaacgggg cccagctgtg      660
288 cggcgggacc ctcatcaata ccatttgggt cgtgtccgcc gctcactgct tcgataagat      720
290 taagaattgg cggaacctca tcgctgtgct cggcgaacac gatctgtccg agcatgacgg      780
292 ggacgaacag tcccgcgggg tggtcaggt catcattccc tccacctatg tgctggcac      840
294 gaccaatcac gatatcgctc tgctccgcct ccaccagccc gtcgtgctca ccgatcacgt      900
296 cgtgcctctg tgctgcctg agcggacctt tagcgaacgc acgctggctt tcgtccgctt      960
298 tagcctcgtg tccggctggg gccagctgct cgaccggggc gctaccgctc tcgagctgat      1020
300 ggtgctcaac gtccccgggc tgatgacca ggactgcctg cagcagtcct gcaaagtggg      1080
302 ggactcccc aatatcacgg agtatatgtt ttgcgctggc tatagcgatg gctccaagga      1140
304 tagctgcaag ggggactccg gcgggccccca tgccacgcac tatcgcgga cctggtacct      1200

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306 caccgggatac gtcagctggg gccagggctg cgccacgggtg gggcactttg gcgtctacac 1260
308 gcgcgtcagc cagtacattg agtggctgca gaagctcatg cggagcgaac cccggcccgg 1320
310 ggtgctcctg cgggcccctt tcccttgata aaagctt 1357
313 <210> SEQ ID NO: 4
314 <211> LENGTH: 31
315 <212> TYPE: DNA
316 <213> ORGANISM: Artificial
318 <220> FEATURE:
319 <223> OTHER INFORMATION: Primer
321 <400> SEQUENCE: 4
322 agctggctag ccactgggca ggtaagtatc a 31
325 <210> SEQ ID NO: 5
326 <211> LENGTH: 31
327 <212> TYPE: DNA
328 <213> ORGANISM: Artificial
330 <220> FEATURE:
331 <223> OTHER INFORMATION: Primer
333 <400> SEQUENCE: 5
334 tggcgggatac cttaagagct gtaattgaac t 31
337 <210> SEQ ID NO: 6
338 <211> LENGTH: 38
339 <212> TYPE: DNA
340 <213> ORGANISM: Artificial
342 <220> FEATURE:
343 <223> OTHER INFORMATION: Primer
345 <400> SEQUENCE: 6
346 cccattctag aaaagcggaa cgccagcaaa ccccaggg 38
349 <210> SEQ ID NO: 7
350 <211> LENGTH: 34
351 <212> TYPE: DNA
352 <213> ORGANISM: Artificial
354 <220> FEATURE:
355 <223> OTHER INFORMATION: Primer
357 <400> SEQUENCE: 7
358 ccaattctta atcttggtga agcagtgagc ggcg 34
361 <210> SEQ ID NO: 8
362 <211> LENGTH: 21
363 <212> TYPE: DNA
364 <213> ORGANISM: Artificial
366 <220> FEATURE:
367 <223> OTHER INFORMATION: Primer
369 <400> SEQUENCE: 8
370 ctccgtgata ttgggggagt c 21
373 <210> SEQ ID NO: 9
374 <211> LENGTH: 34
375 <212> TYPE: DNA
376 <213> ORGANISM: Artificial
378 <220> FEATURE:
379 <223> OTHER INFORMATION: Primer

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 11/16/2006
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Input Set : A:\0272wo310.ST25.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19

VERIFICATION SUMMARY

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Input Set : A:\0272wo310.ST25.txt

Output Set: N:\CRF4\11162006\J549506.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date